

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: WALLACH, David
BIGDA, Jacek
BELETSKY, Igor
METT, Igor
- (ii) TITLE OF INVENTION: TNF LIGANDS
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BROWDY AND NEIMARK
 - (B) STREET: 419 Seventh Street, N.W.
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/115,685
 - (B) FILING DATE: 03-SEP-1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: IL 103051
 - (B) FILING DATE: 03-SEP-1992
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: IL 106271
 - (B) FILING DATE: 08-JUL-1993
- (ix) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Townsend, G. Kevin
 - (B) REGISTRATION NUMBER: 34,033
 - (C) REFERENCE/DOCKET NUMBER: WALLACH=10
- (x) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-628-5197
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Gln Val Phe Thr Thr His Gln Ile Cys Asn Val Val Ala Ile Pro
1 5 10 15

Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Val
20 25 30
Asp Phe Ala Leu Pro Val Gly Leu Ile Cys Asn Val Val Ala Ile Pro
35 40 45
Gly Asn Ala Ser Met Asp Ala Val Cys Thr
50 55

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 90..1472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCAGAGCGCAG CGGAGCCTGG AGAGAAGGCG CTGGGCTGCG AGGGCGCGAG GGCGCGAGGG	60
CAGGGGGCAA CCGGACCCCG CCCGCACCC ATG GCG CCC GTC GCC GTC TGG GCC	113
Met Ala Pro Val Ala Val Trp Ala	
1 5	
GCG CTG GCC GTC GGA CTG GAG CTC TGG GCT GCG GCG CAC GCC TTG CCC	161
Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro	
10 15 20	
GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG CCC GGG AGC ACA TGC	209
Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys	
25 30 35 40	
CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC AGC AAA	257
Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys	
45 50 55	
TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC TCG GAC	305
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp	
60 65 70	
ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC TGG AAC	353
Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn	
75 80 85	
TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC TGT AGC TCT GAC CAG	401
Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln	
90 95 100	
GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC CGC ATC TGC ACC TGC	449
Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys	
105 110 115 120	
AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG GAG GGG TGC CGG CTG	497
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu	
125 130 135	
TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC GGC GTG GCC AGA CCA	545
Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro	
140 145 150	
GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC TGT GCC CCG GGG ACG	593

Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr		
		155					160					165					
TTC	TCC	AAC	ACG	ACT	TCA	TCC	ACG	GAT	ATT	TGC	AGG	CCC	CAC	CAG	ATC	641	
Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	Asp	Ile	Cys	Arg	Pro	His	Gln	Ile		
	170					175				180							
TGT	AAC	GTG	GTG	GCC	ATC	CCT	GGG	AAT	GCA	AGC	ATG	GAT	GCA	GTC	TGC	689	
Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser	Met	Asp	Ala	Val	Cys		
185					190					195				200			
ACG	TCC	ACG	TCC	CCC	ACC	CGG	AGT	ATG	GCC	CCA	GGG	GCA	GTA	CAC	TTA	737	
Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	Met	Ala	Pro	Gly	Ala	Val	His	Leu		
				205					210					215			
CCC	CAG	CCA	GTG	TCC	ACA	CGA	TCC	CAA	CAC	ACG	CAG	CCA	ACT	CCA	GAA	785	
Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	Gln	His	Thr	Gln	Pro	Thr	Pro	Glu		
			220					225					230				
CCC	AGC	ACT	GCT	CCA	AGC	ACC	TCC	TTC	CTG	CTC	CCA	ATG	GGC	CCC	AGC	833	
Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser		
	235						240					245					
CCC	CCA	GCT	GAA	GGG	AGC	ACT	GGC	GAC	TTC	GCT	CTT	CCA	GTT	GGA	CTG	881	
Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu		
	250					255					260						
ATT	GTG	GGT	GTG	ACA	GCC	TTG	GGT	CTA	CTA	ATA	ATA	GGA	GTG	GTG	AAC	929	
Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn		
265					270					275					280		
TGT	GTC	ATC	ATG	ACC	CAG	GTG	AAA	AAG	AAG	CCC	TTG	TGC	CTG	CAG	AGA	977	
Cys	Val	Ile	Met	Thr	Gln	Val	Lys	Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg		
				285				290						295			
GAA	GCC	AAG	GTG	CCT	CAC	TTG	CCT	GCC	GAT	AAG	GCC	CGG	GGT	ACA	CAG	1025	
Glu	Ala	Lys	Val	Pro	His	Leu	Pro	Ala	Asp	Lys	Ala	Arg	Gly	Thr	Gln		
			300					305					310				
GGC	CCC	GAG	CAG	CAG	CAC	CTG	CTG	ATC	ACA	GCG	CCG	AGC	TCC	AGC	AGC	1073	
Gly	Pro	Glu	Gln	Gln	His	Leu	Leu	Ile	Thr	Ala	Pro	Ser	Ser	Ser	Ser		
		315					320					325					
AGC	TCC	CTG	GAG	AGC	TCG	GCC	AGT	GCG	TTG	GAC	AGA	AGG	GCG	CCC	ACT	1121	
Ser	Ser	Leu	Glu	Ser	Ser	Ala	Ser	Ala	Leu	Asp	Arg	Arg	Ala	Pro	Thr		
	330					335					340						
CGG	AAC	CAG	CCA	CAG	GCA	CCA	GGC	GTG	GAG	GCC	AGT	GGG	GCC	GGG	GAG	1169	
Arg	Asn	Gln	Pro	Gln	Ala	Pro	Gly	Val	Glu	Ala	Ser	Gly	Ala	Gly	Glu		
345					350					355					360		
GCC	CGG	GCC	AGC	ACC	GGG	AGC	TCA	GAT	TCT	TCC	CCT	GGT	GGC	CAT	GGG	1217	
Ala	Arg	Ala	Ser	Thr	Gly	Ser	Ser	Asp	Ser	Ser	Pro	Gly	Gly	His	Gly		
				365				370						375			
ACC	CAG	GTC	AAT	GTC	ACC	TGC	ATC	GTG	AAC	GTC	TGT	AGC	AGC	TCT	GAC	1265	
Thr	Gln	Val	Asn	Val	Thr	Cys	Ile	Val	Asn	Val	Cys	Ser	Ser	Ser	Asp		
			380					385					390				
CAC	AGC	TCA	CAG	TGC	TCC	TCC	CAA	GCC	AGC	TCC	ACA	ATG	GGA	GAC	ACA	1313	
His	Ser	Ser	Gln	Cys	Ser	Ser	Gln	Ala	Ser	Ser	Thr	Met	Gly	Asp	Thr		
			395				400					405					
GAT	TCC	AGC	CCC	TCG	GAG	TCC	CCG	AAG	GAC	GAG	CAG	GTC	CCC	TTC	TCC	1361	
Asp	Ser	Ser	Pro	Ser	Glu	Ser	Pro	Lys	Asp	Glu	Gln	Val	Pro	Phe	Ser		
	410					415					420						
AAG	GAG	GAA	TGT	GCC	TTT	CGG	TCA	CAG	CTG	GAG	ACG	CCA	GAG	ACC	CTG	1409	
Lys	Glu	Glu	Cys	Ala	Phe	Arg	Ser	Gln	Leu	Glu	Thr	Pro	Glu	Thr	Leu		
425					430					435					440		

CTG GGG AGC ACC GAA GAG AAG CCC CTG CCC CTT GGA GTG CCT GAT GCT	1457
Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala	
445 450 455	
GGG ATG AAG CCC AGT TAACCAGGCC GGTGTGGGCT GTGTCGTAGC CAAGGTGGGC	1512
Gly Met Lys Pro Ser	
460	
TGAGCCCTGG CAGGATGACC CTGCGAAGGG GCCCTGGTCC TTCCAGGCCC CCACCACTAG	1572
GACTCTGAGG CTCTTTCTGG GCCAAGTTCC TCTAGTGCCC TCCACAGCCG CAGCCTCCCT	1632
CTGACCTGCA GGCCAAGAGC AGAGGCAGCG AGTTGGGGAA AGCCTCTGCT GCCATGGTGT	1692
GTCCCTCTCG GAAGGCTGGC TGGGCATGGA CGTTCGGGGC ATGCTGGGGC AAGTCCCTGA	1752
CTCTCTGTGA CCTGCCCCGC CCAGCTGCAC CTGCCAGCCT GGCTTCTGGA GCCCTTGGGT	1812
TTTTTGTTTG TTTGTTTGT TGTGTGTTTG TTTCTCCCCC TGGGCTCTGC CCAGCTCTGG	1872
CTTCAGAAA ACCCCAGCAT CCTTTTCTGC AGAGGGGCTT TCTGGAGAGG AGGGATGCTG	1932
CCTGAGTCAC CCATGAAGAC AGGACAGTGC TTCAGCCTGA GGCTGAGACT GCGGGATGGT	1992
CCTGGGGCTC TGTGTAGGGA GGAGGTGGCA GCCCTGTAGG GAACGGGGTC CTTCAAGTTA	2052
GCTCAGGAGG CTTGGAAAGC ATCACCTCAG GCCAGGTGCA GTGGCTCAGC CCTATGATCC	2112
CAGCACTTTG GGAGGCTGAG GCGGGTGGAT CACCTGAGGT TAGGAGTTCG AGACCAGCCT	2172
GGCCAACATG GTAAAACCCC ATCTCTACTA AAAATACAGA AATTAGCCGG GC	2224

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 461 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ala	Pro	Val	Ala	Val	Trp	Ala	Ala	Leu	Ala	Val	Gly	Leu	Glu	Leu
1				5					10					15	
Trp	Ala	Ala	Ala	His	Ala	Leu	Pro	Ala	Gln	Val	Ala	Phe	Thr	Pro	Tyr
			20					25					30		
Ala	Pro	Glu	Pro	Gly	Ser	Thr	Cys	Arg	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln
			35				40					45			
Thr	Ala	Gln	Met	Cys	Cys	Ser	Lys	Cys	Ser	Pro	Gly	Gln	His	Ala	Lys
			50				55				60				
Val	Phe	Cys	Thr	Lys	Thr	Ser	Asp	Thr	Val	Cys	Asp	Ser	Cys	Glu	Asp
	65				70					75				80	
Ser	Thr	Tyr	Thr	Gln	Leu	Trp	Asn	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys
				85					90					95	
Gly	Ser	Arg	Cys	Ser	Ser	Asp	Gln	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg
			100					105					110		
Glu	Gln	Asn	Arg	Ile	Cys	Thr	Cys	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu
		115					120					125			
Ser	Lys	Gln	Glu	Gly	Cys	Arg	Leu	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg

130					135					140					
Pro	Gly	Phe	Gly	Val	Ala	Arg	Pro	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val
145					150					155					160
Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr
				165					170					175	
Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly
			180					185					190		
Asn	Ala	Ser	Met	Asp	Ala	Val	Cys	Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser
			195				200					205			
Met	Ala	Pro	Gly	Ala	Val	His	Leu	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser
	210					215					220				
Gln	His	Thr	Gln	Pro	Thr	Pro	Glu	Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser
	225					230					235				240
Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly
				245					250					255	
Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	Ile	Val	Gly	Val	Thr	Ala	Leu	Gly
			260					265					270		
Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	Cys	Val	Ile	Met	Thr	Gln	Val	Lys
		275					280					285			
Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	Glu	Ala	Lys	Val	Pro	His	Leu	Pro
	290					295					300				
Ala	Asp	Lys	Ala	Arg	Gly	Thr	Gln	Gly	Pro	Glu	Gln	Gln	His	Leu	Leu
	305					310					315				320
Ile	Thr	Ala	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Glu	Ser	Ser	Ala	Ser
				325					330					335	
Ala	Leu	Asp	Arg	Arg	Ala	Pro	Thr	Arg	Asn	Gln	Pro	Gln	Ala	Pro	Gly
			340					345					350		
Val	Glu	Ala	Ser	Gly	Ala	Gly	Glu	Ala	Arg	Ala	Ser	Thr	Gly	Ser	Ser
		355					360					365			
Asp	Ser	Ser	Pro	Gly	Gly	His	Gly	Thr	Gln	Val	Asn	Val	Thr	Cys	Ile
	370					375					380				
Val	Asn	Val	Cys	Ser	Ser	Ser	Asp	His	Ser	Ser	Gln	Cys	Ser	Ser	Gln
	385					390					395				400
Ala	Ser	Ser	Thr	Met	Gly	Asp	Thr	Asp	Ser	Ser	Pro	Ser	Glu	Ser	Pro
				405					410					415	
Lys	Asp	Glu	Gln	Val	Pro	Phe	Ser	Lys	Glu	Glu	Cys	Ala	Phe	Arg	Ser
			420					425					430		
Gln	Leu	Glu	Thr	Pro	Glu	Thr	Leu	Leu	Gly	Ser	Thr	Glu	Glu	Lys	Pro
		435					440					445			
Leu	Pro	Leu	Gly	Val	Pro	Asp	Ala	Gly	Met	Lys	Pro	Ser			
	450					455					460				

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTG	AAA	CTG	CAG	GAG	TCT	GGA	CCT	GAG	CTG	GTG	AAG	CCT	GGG	GCC	TCA	48
Val	Lys	Leu	Gln	Glu	Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	
1				5					10					15		
GTG	AAG	ATT	TCC	TGC	AAA	ACT	TCT	GGC	TTC	GCA	TTC	AGT	CAT	TCT	TGG	96
Val	Lys	Ile	Ser	Cys	Lys	Thr	Ser	Gly	Phe	Ala	Phe	Ser	His	Ser	Trp	
			20					25					30			
ATG	AAC	TGG	GTG	AGG	CAG	AGG	CCT	GGA	CAG	GGT	CTT	GAA	TGG	ATT	GGA	144
Met	Asn	Trp	Val	Arg	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	
			35				40					45				
CGG	ATT	TAT	CCT	GGA	GAT	GGA	AAT	ACT	GAT	TAC	CCT	GGG	AAG	TTC	CAG	192
Arg	Ile	Tyr	Pro	Gly	Asp	Gly	Asn	Thr	Asp	Tyr	Pro	Gly	Lys	Phe	Gln	
	50					55					60					
GGC	CAG	GCC	ACA	CTG	ACT	GCA	GAC	AAA	TCT	TCC	AGC	ACA	GCC	TAC	ATG	240
Gly	Gln	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	
65					70				75						80	
CAA	CTC	TTC	AGT	CTG	ACC	TCT	GTG	GAC	TCT	GCG	GTC	TAT	TTT	TGT	GCA	288
Gln	Leu	Phe	Ser	Leu	Thr	Ser	Val	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Ala	
				85					90					95		
CCC	GGC	CGT	TGG	TAC	CTC	GAA	GTC	TGG	GGC	CAA	GGG	ACC	ACG	GTC	ACC	336
Pro	Gly	Arg	Trp	Tyr	Leu	Glu	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	
			100					105					110			
GTC	TCC	TCA														345
Val	Ser	Ser														
			115													

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val	Lys	Leu	Gln	Glu	Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser
1				5					10					15	
Val	Lys	Ile	Ser	Cys	Lys	Thr	Ser	Gly	Phe	Ala	Phe	Ser	His	Ser	Trp
			20					25					30		
Met	Asn	Trp	Val	Arg	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly
			35				40					45			
Arg	Ile	Tyr	Pro	Gly	Asp	Gly	Asn	Thr	Asp	Tyr	Pro	Gly	Lys	Phe	Gln
	50					55					60				
Gly	Gln	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met
65					70				75						80

Gln Leu Phe Ser Leu Thr Ser Val Asp Ser Ala Val Tyr Phe Cys Ala
85 90 95
Pro Gly Arg Trp Tyr Leu Glu Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110
Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCT GAG CTG GTG GCT CCT GGG GCC TCA GTG AAG ATT TCC TGC AAA GCT	48
Pro Glu Leu Val Ala Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala	
1 5 10 15	
TCT GGC TAC GCA TTC AGT CAC TCT TGG ATG AAC TGG GTG AAG CAG AGG	96
Ser Gly Tyr Ala Phe Ser His Ser Trp Met Asn Trp Val Lys Gln Arg	
20 25 30	
CCT GGA AAG GGT CTT GAG TGG ATT GGA CGG ATT CAT CCT GGA GAT GGA	144
Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Ile His Pro Gly Asp Gly	
35 40 45	
GAC ACT GAC TAC AAT GGG AAC TTC AGG GGC AAG GCC ACA CTG ACT GCA	192
Asp Thr Asp Tyr Asn Gly Asn Phe Arg Gly Lys Ala Thr Leu Thr Ala	
50 55 60	
GAC ACA TCC TCC AGC TCA GCC TAC ATG CAG CTC AGC AGC CTG ACC TCT	240
Asp Thr Ser Ser Ser Ser Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser	
65 70 75 80	
GTG GAT TCT GCG GTC TAC TTC TGT GCA CCC GGC CGT TGG TAC CTC GAG	288
Val Asp Ser Ala Val Tyr Phe Cys Ala Pro Gly Arg Trp Tyr Leu Glu	
85 90 95	
GTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA	324
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
100 105	

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro Glu Leu Val Ala Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala
1 5 10 15

Ser Gly Tyr Ala Phe Ser His Ser Trp Met Asn Trp Val Lys Gln Arg
20 25 30
Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Ile His Pro Gly Asp Gly
35 40 45
Asp Thr Asp Tyr Asn Gly Asn Phe Arg Gly Lys Ala Thr Leu Thr Ala
50 55 60
Asp Thr Ser Ser Ser Ser Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
65 70 75 80
Val Asp Ser Ala Val Tyr Phe Cys Ala Pro Gly Arg Trp Tyr Leu Glu
85 90 95
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
100 105

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTG TCC CTG CAG GAG TCT GGG GGA GGC TTA GTG CAG CCT GGA GGG TCC	48
Val Ser Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser	
1 5 10 15	
CGG AAA CTC TCC TGT GCA GCT TCT GGA TTC ACT TTC AGT AGC TTT GGA	96
Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe Gly	
20 25 30	
ATG CAC TGG GTT CGT CAG GCT CCA GAG AAG GGG CTG GAG TGG GTC GCA	144
Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val Ala	
35 40 45	
TAC ATT AGT AGT GGC AGT AGT ACC CTC CAC TAT GCA GAC ACA GTG AAG	192
Tyr Ile Ser Ser Gly Ser Ser Thr Leu His Tyr Ala Asp Thr Val Lys	
50 55 60	
GGC CGA TTC ACC ATC TCC AGA GAC AAT CCC AAG AAC ACG CTG TTC CTG	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn Thr Leu Phe Leu	
65 70 75 80	
CAA ATG AAA CTA CCC TCA CTA TGC TAT GGA CTA CTG GGG CCA AGG GAC	288
Gln Met Lys Leu Pro Ser Leu Cys Tyr Gly Leu Leu Gly Pro Arg Asp	
85 90 95	
CAC GGT CAC CGT CTC CTC A	307
His Gly His Arg Leu Leu	
100	

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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Val Ser Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
 1           5           10           15
Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe Gly
          20           25           30
Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val Ala
          35           40           45
Tyr Ile Ser Ser Gly Ser Ser Thr Leu His Tyr Ala Asp Thr Val Lys
          50           55           60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn Thr Leu Phe Leu
          65           70           75           80
Gln Met Lys Leu Pro Ser Leu Cys Tyr Gly Leu Leu Gly Pro Arg Asp
          85           90           95
His Gly His Arg Leu Leu
          100

```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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TCC TCC CTG GCT ATG TCA GTA GGA CAG ATG GTC ACT ATG AGC TGC AAG      48
Ser Ser Leu Ala Met Ser Val Gly Gln Met Val Thr Met Ser Cys Lys
 1           5           10           15

TCC AGT CAG AGC CTT TTA ACT AGT AGC ACT CAA AAG AAC TCT TTG GCC      96
Ser Ser Gln Ser Leu Leu Thr Ser Ser Thr Gln Lys Asn Ser Leu Ala
          20           25           30

TGG TAC CAG CAG ACA CCA GGA CAG TCT CCT AAA CTT CTG ATA TAC TTT     144
Trp Tyr Gln Gln Thr Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Phe
          35           40           45

GCA TCC ACT AGG CTA TCT GGG GTC CCT GAT CGC TTC ATA GGC AGT GGA     192
Ala Ser Thr Arg Leu Ser Gly Val Pro Asp Arg Phe Ile Gly Ser Gly
          50           55           60

TCT GGG ACA GAT TTC ACT CTT ACC ATC AGC AGT GTG CAG GCT GAA GAC     240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp
          65           70           75           80

CTG GCA GAT TAC TTC TGT CAG CAA CAT TAT AGC ACT CCA TTT ACG TTC     288
Leu Ala Asp Tyr Phe Cys Gln Gln His Tyr Ser Thr Pro Phe Thr Phe
          85           90           95

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GGC TCG GGG ACA AAG TTG GAA ATA GAG CGG GCT GAT GCT GCA CCA ACT 336
 Gly Ser Gly Thr Lys Leu Glu Ile Glu Arg Ala Asp Ala Ala Pro Thr
 100 105 110

GTA TCC ATC TTC CCA CCA TCC A 358
 Val Ser Ile Phe Pro Pro Ser
 115

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Ser Leu Ala Met Ser Val Gly Gln Met Val Thr Met Ser Cys Lys
 1 5 10 15
 Ser Ser Gln Ser Leu Leu Thr Ser Ser Thr Gln Lys Asn Ser Leu Ala
 20 25 30
 Trp Tyr Gln Gln Thr Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Phe
 35 40 45
 Ala Ser Thr Arg Leu Ser Gly Val Pro Asp Arg Phe Ile Gly Ser Gly
 50 55 60
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp
 65 70 75 80
 Leu Ala Asp Tyr Phe Cys Gln Gln His Tyr Ser Thr Pro Phe Thr Phe
 85 90 95
 Gly Ser Gly Thr Lys Leu Glu Ile Glu Arg Ala Asp Ala Ala Pro Thr
 100 105 110
 Val Ser Ile Phe Pro Pro Ser
 115

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys
 1 5 10 15
 Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly
 20 25 30
 Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
 35 40 45
 Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg
 50 55 60

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp
 65 70 75 80
 Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu
 85 90 95
 Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val
 100 105 110
 His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala
 115 120 125
 Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys
 130 135 140
 Lys Ser Leu Glu Cys Thr Lys Leu Cys
 145 150

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
 1 5 10 15
 Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
 20 25 30
 Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
 35 40 45
 Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Asp
 50 55 60
 Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
 65 70 75 80
 Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
 85 90 95
 Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
 100 105 110
 Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
 115 120 125
 Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
 130 135 140
 Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
 145 150 155 160
 Val Cys Thr

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid

Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu
 130 135 140

Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu
 145 150 155

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Cys Arg Glu Lys Gln Tyr Leu Ile Asn Ser Gln Cys Cys Ser Leu
 1 5 10 15

Cys Gln Pro Gly Gln Lys Leu Val Ser Asp Cys Thr Glu Phe Thr Glu
 20 25 30

Thr Glu Cys Leu Pro Cys Gly Glu Ser Glu Phe Leu Asp Thr Trp Asn
 35 40 45

Arg Glu Thr His Cys His Gln His Lys Tyr Cys Asp Pro Asn Leu Gly
 50 55 60

Leu Arg Val Gln Gln Lys Gly Thr Ser Glu Thr Asp Thr Ile Cys Thr
 65 70 75 80

Cys Glu Glu Gly Trp His Cys Thr Ser Glu Ala Cys Glu Ser Cys Val
 85 90 95

Leu His Arg Ser Cys Ser Pro Gly Phe Gly Val Lys Gln Ile Ala Thr
 100 105 110

Gly Val Ser Asp Thr Ile Cys Glu Pro Cys Pro Val Gly Phe Phe Ser
 115 120 125

Asn Val Ser Ser Ala Phe Glu Lys Cys His Pro Thr Ser Cys Glu Thr
 130 135 140

Lys Asp Leu Val Val Gln Gln Ala Gly Thr Asn Lys Thr Asp Val Val
 145 150 155 160

Cys Gly

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asn Cys Val Lys Asp Thr Tyr Pro Ser Gly His Lys Cys Cys Arg Glu
 1 5 10 15

Cys	Gln	Pro	Gly	His	Gly	Met	Val	Ser	Arg	Cys	Asp	His	Thr	Arg	Asp
			20					25					30		
Thr	Val	Cys	His	Pro	Cys	Glu	Pro	Gly	Phe	Tyr	Asn	Glu	Ala	Val	Asn
		35					40					45			
Tyr	Asp	Thr	Cys	Lys	Gln	Cys	Thr	Gln	Cys	Asn	His	Arg	Ser	Gly	Ser
	50					55					60				
Glu	Leu	Lys	Gln	Asn	Cys	Thr	Pro	Thr	Glu	Asp	Thr	Val	Cys	Gln	Cys
65					70					75					80
Arg	Pro	Gly	Thr	Gln	Pro	Arg	Gln	Asp	Ser	Ser	His	Lys	Leu	Gly	Val
				85					90					95	
Asp	Cys	Val	Pro	Cys	Pro	Pro	Gly	His	Phe	Ser	Pro	Gly	Ser	Asn	Gln
			100					105					110		
Ala	Cys	Lys	Pro	Trp	Thr	Asn	Cys	Thr	Leu	Ser	Gly	Lys	Gln	Ile	Arg
		115					120					125			
His	Pro	Ala	Ser	Asn	Ser	Leu	Asp	Thr	Val	Cys	Glu				
	130					135					140				